












FastQC Report

Summary

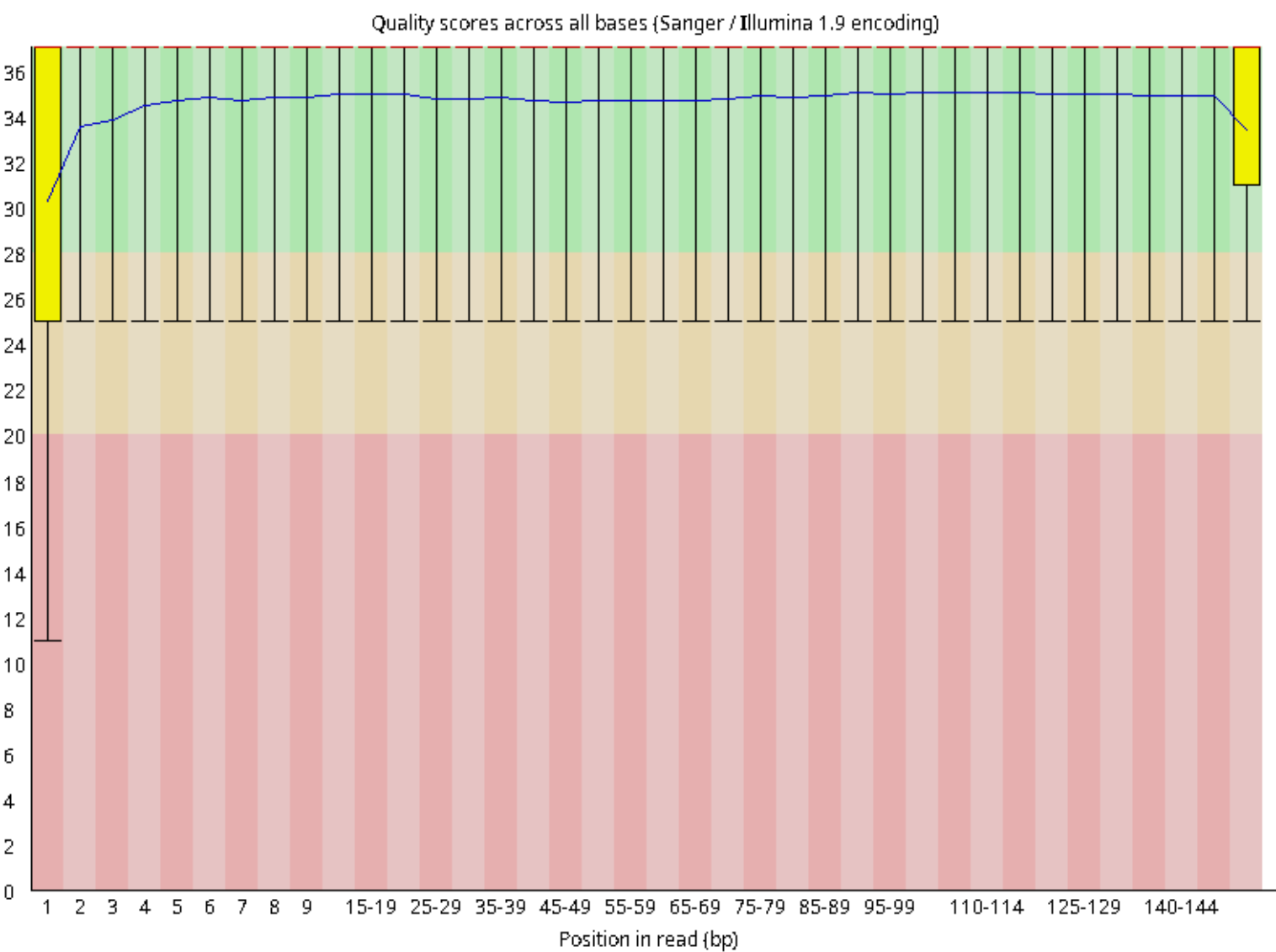
Fri 15 Aug 2025
SRR33784444_1_unpaired.fastq

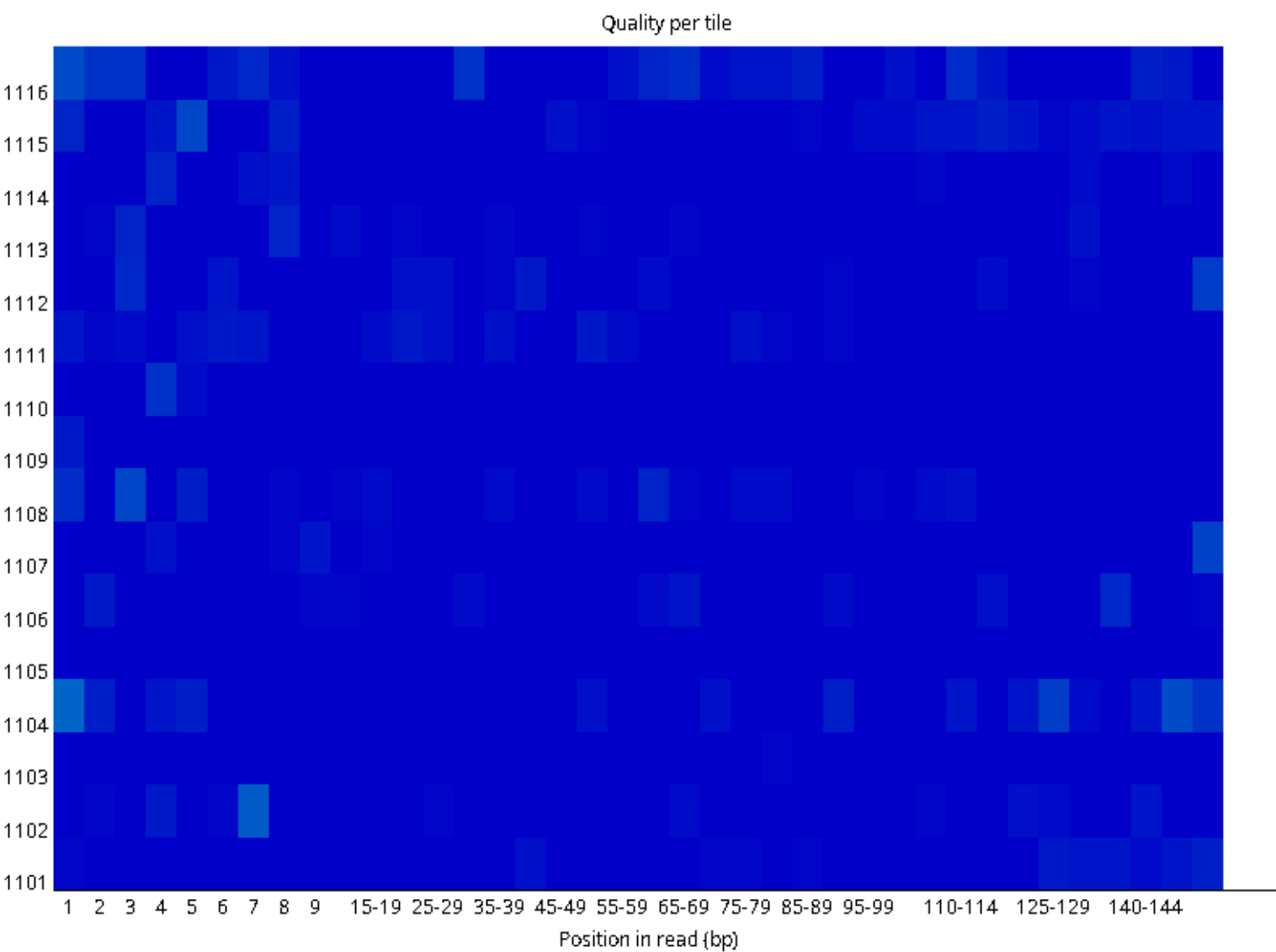
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Basic Statistics

Measure	Value
Filename	SRR33784444_1_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	13728
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	45

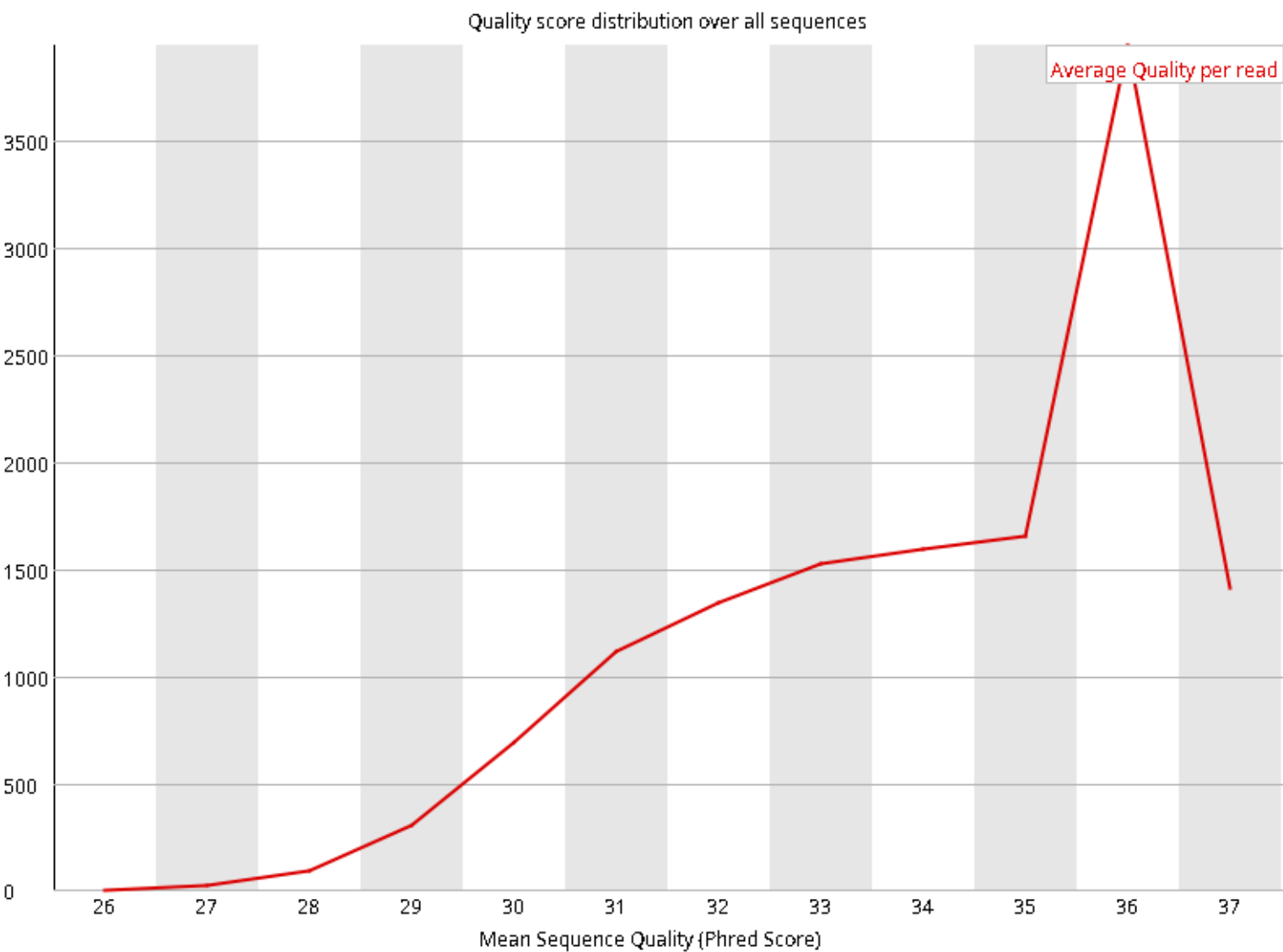
✔ Per base sequence quality



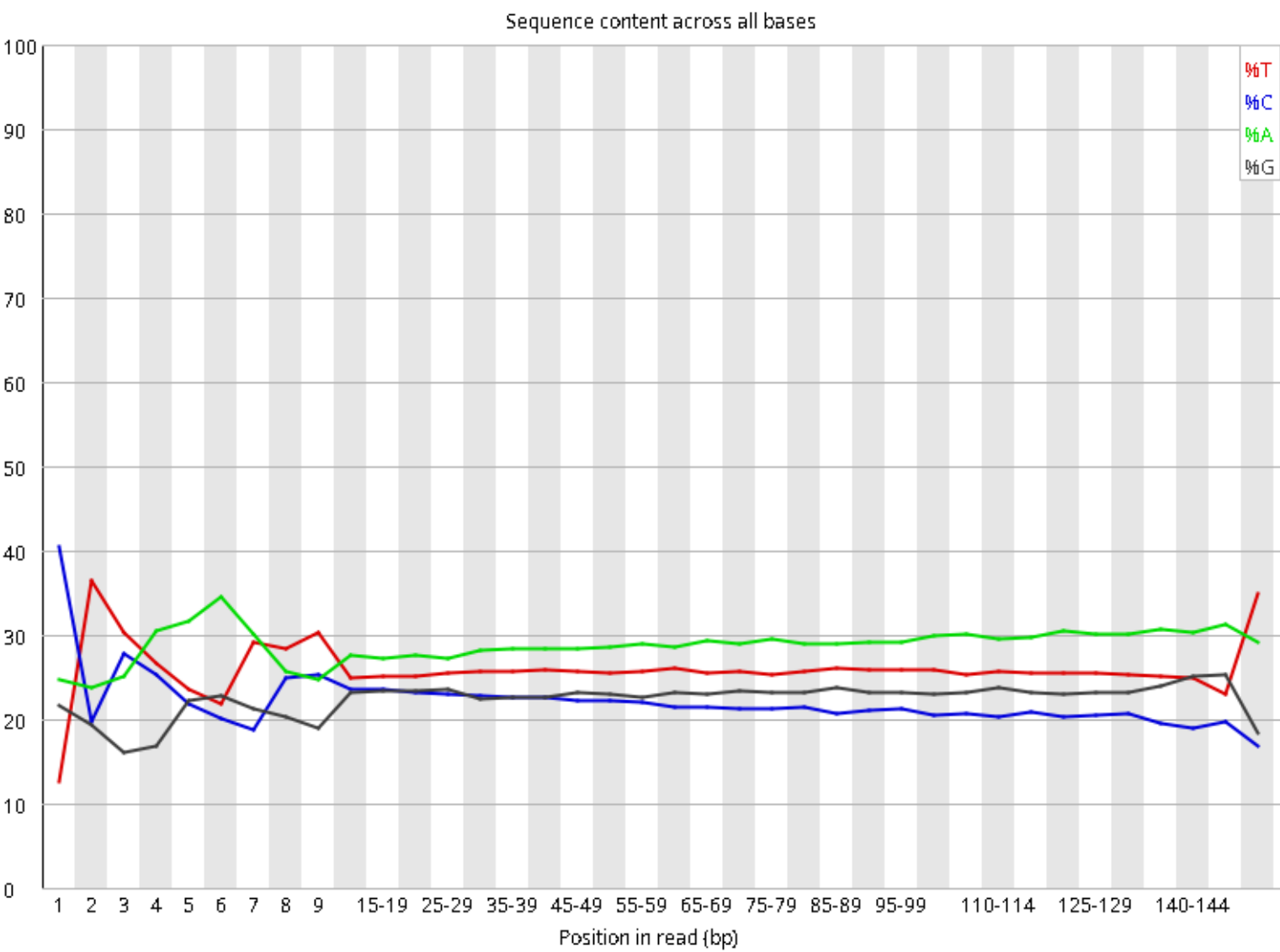




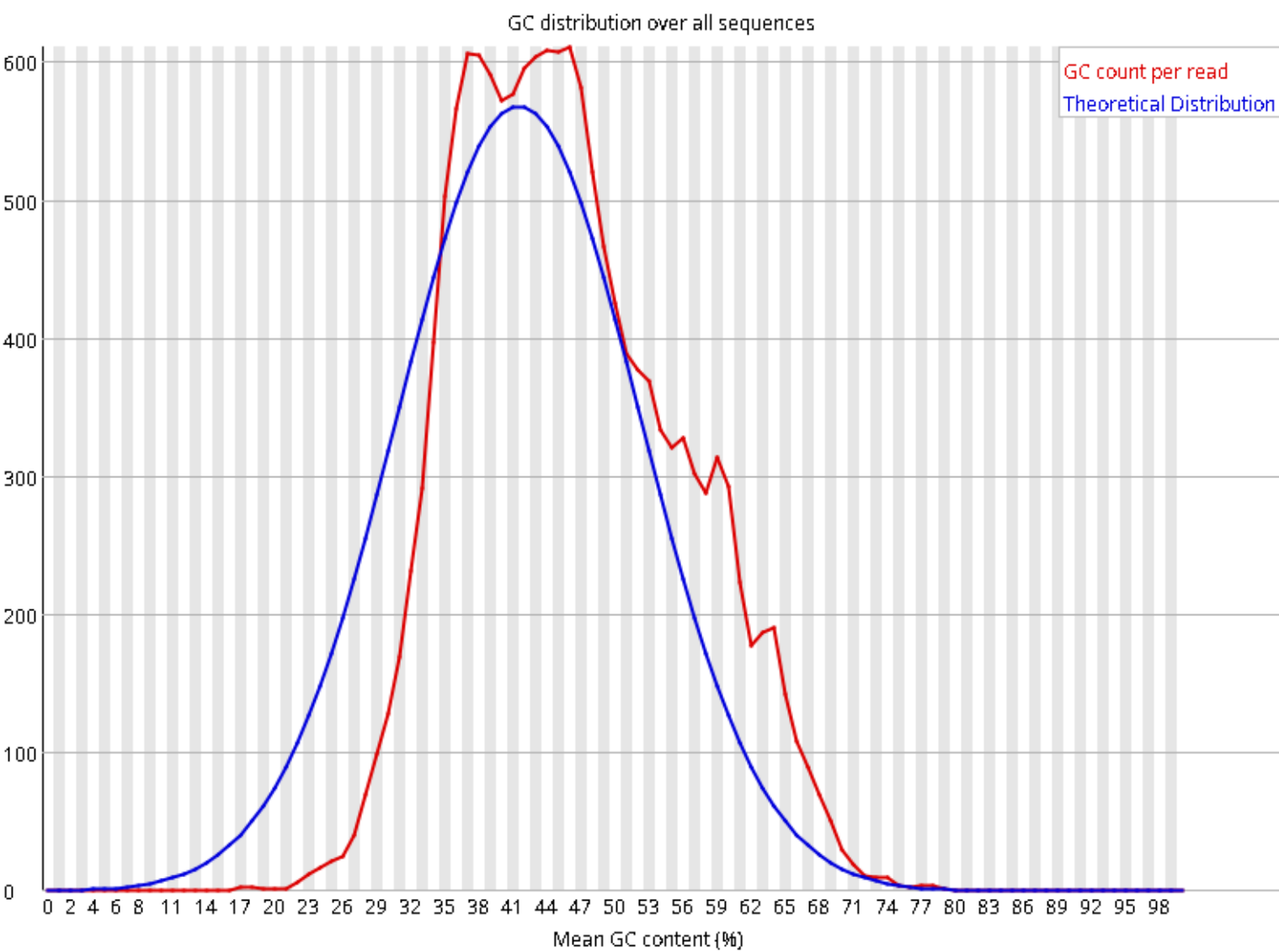
Per sequence quality scores



! Per base sequence content

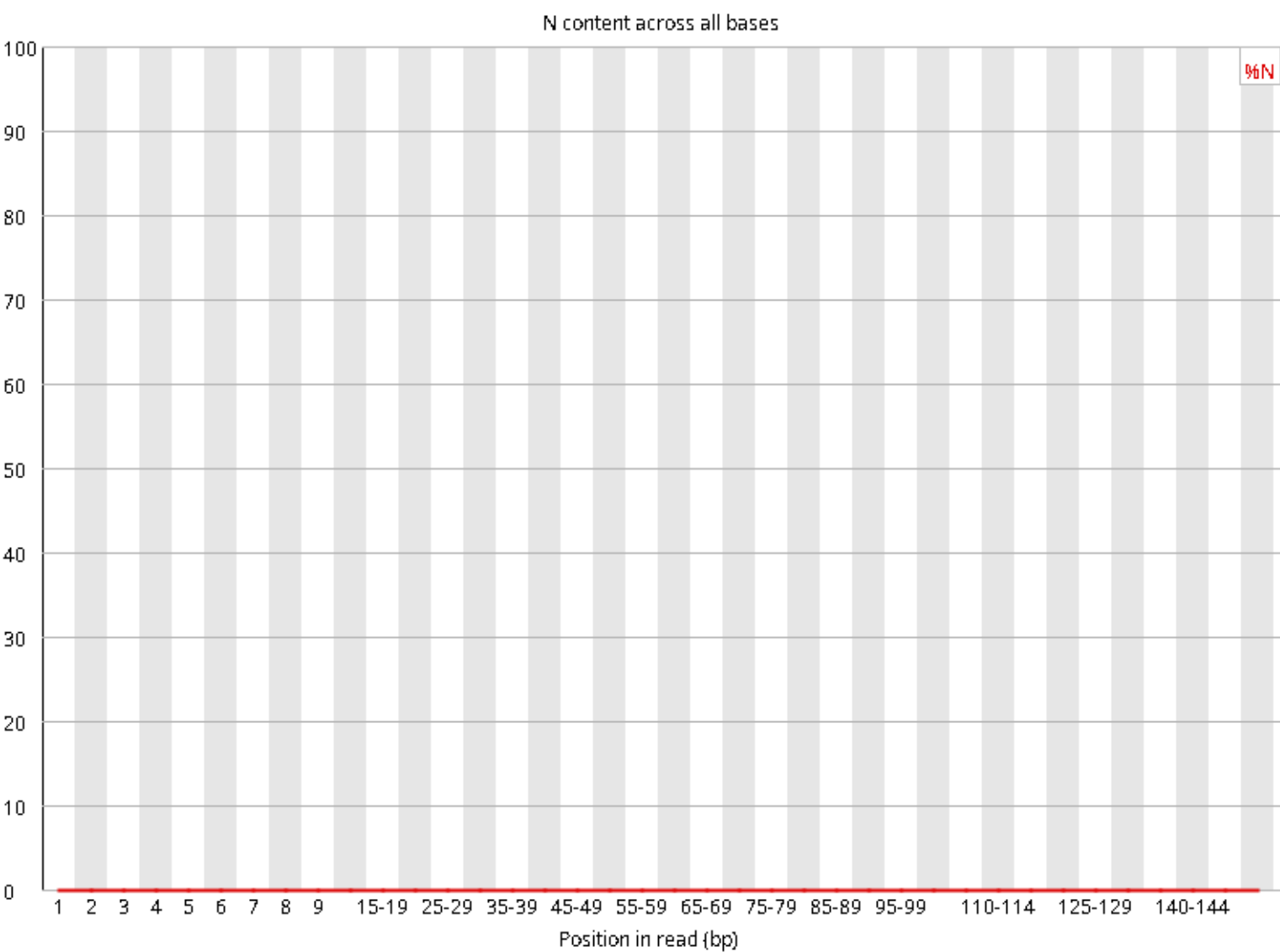


❌ Per sequence GC content

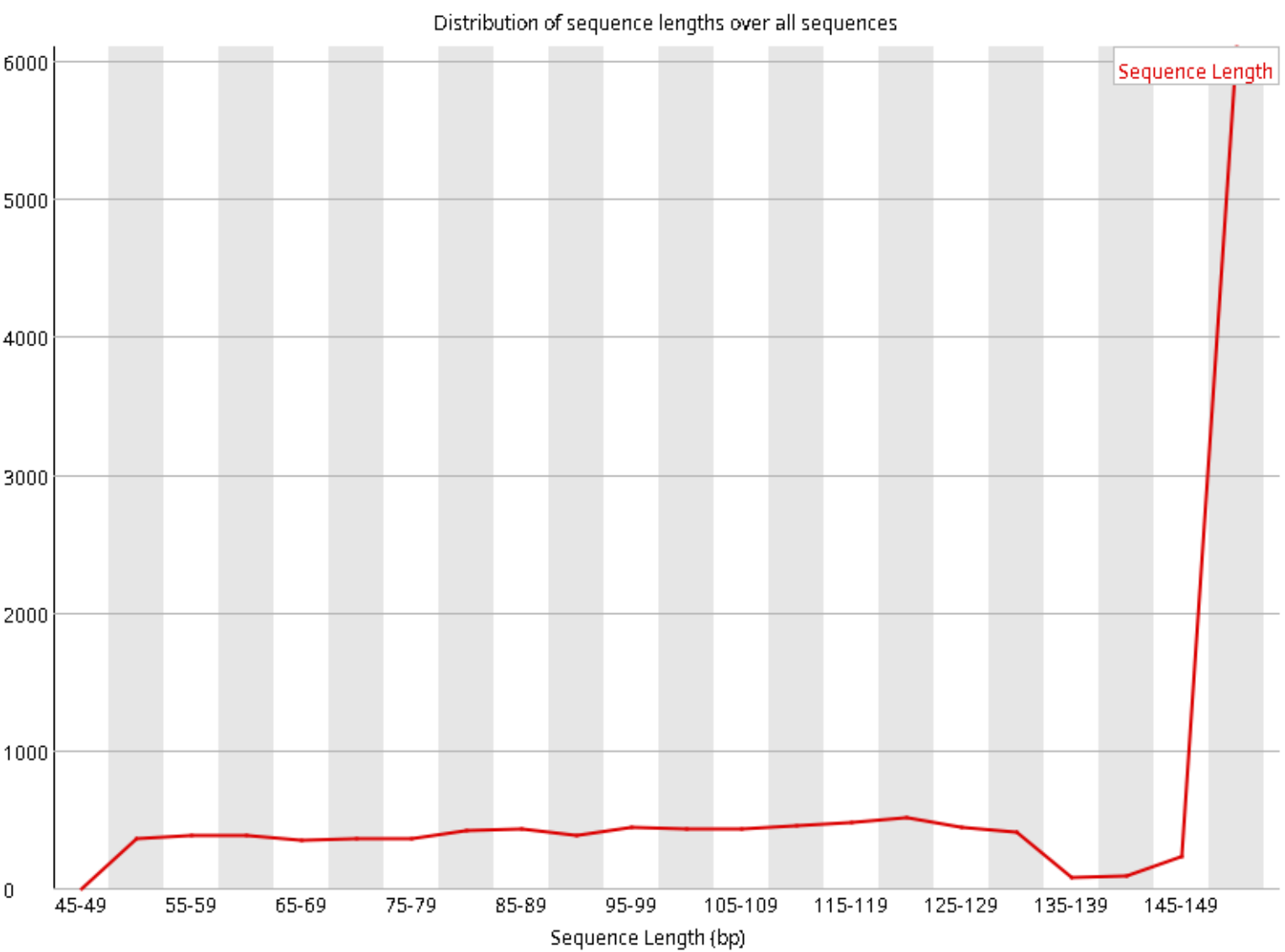




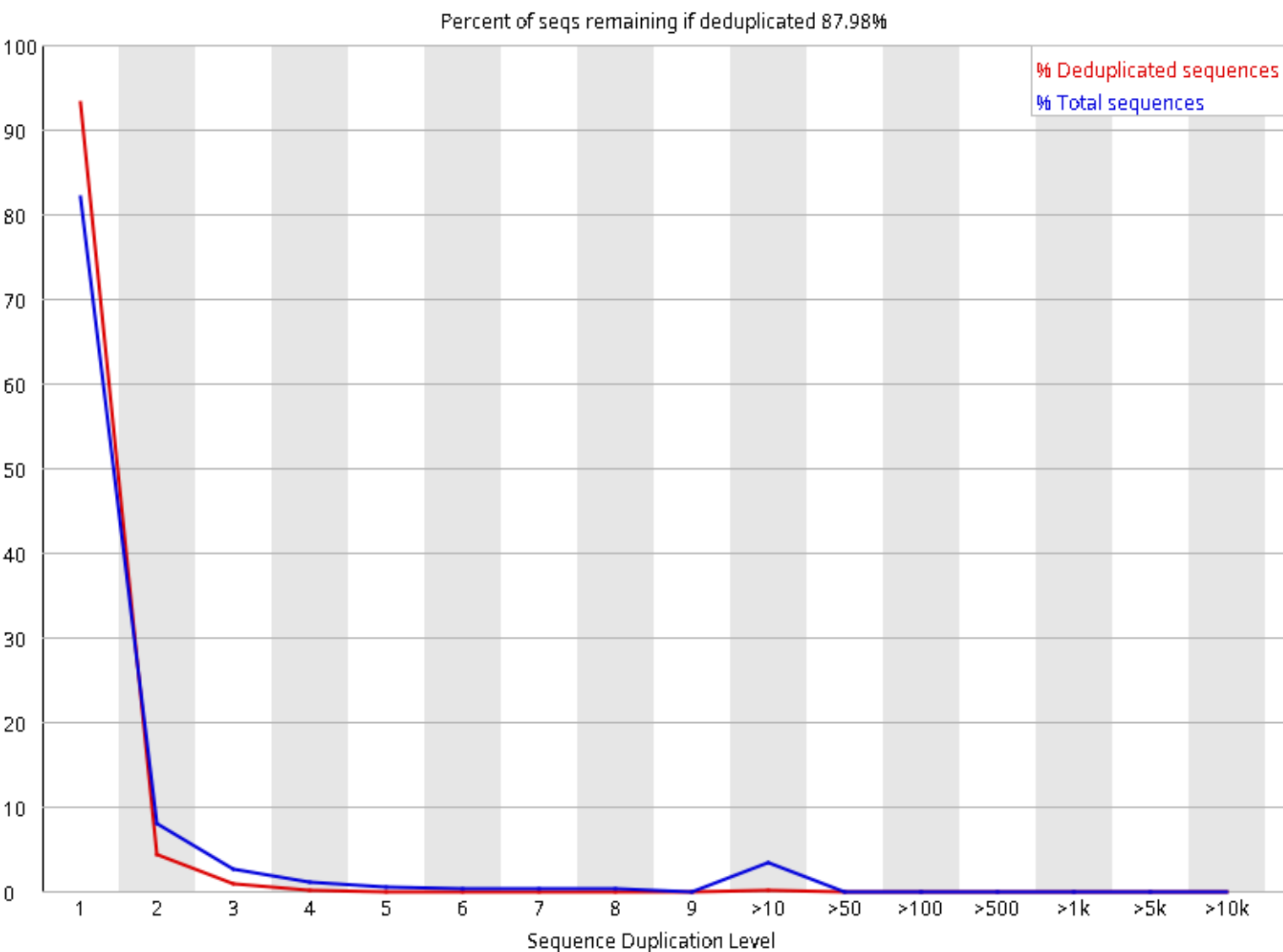
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGG	27	0.1966783216783217	No Hit
CCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAG	27	0.1966783216783217	No Hit
AGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAGCAG	25	0.1821095571095571	No Hit
CTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATA	25	0.1821095571095571	No Hit
CCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAA	24	0.17482517482517482	No Hit
CTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGG	21	0.15297202797202797	No Hit
CCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGA	21	0.15297202797202797	No Hit
CACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGGAG	20	0.1456876456876457	No Hit
AGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAA	20	0.1456876456876457	No Hit

Sequence	Count	Percentage	Possible Source
CTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGA	19	0.1384032634032634	No Hit
ATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAAATTTACCAG	18	0.13111888111888112	No Hit
GTCACAGTAAAAATAGGGGGACAGCTAATAGAAGCTCTATTAGACACAGG	18	0.13111888111888112	No Hit
GCTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAAC	18	0.13111888111888112	No Hit
CTAATAGAAGCTCTATTAGACACAGGAGCAGATGATACAGTATTAGAACA	16	0.11655011655011654	No Hit
AGAGTTACCACCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCT	14	0.10198135198135197	No Hit
CTATTAGACACAGGAGCAGATGATACAGTATTAGAACAAATAAATTTACC	14	0.10198135198135197	No Hit
TACCACCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCA	14	0.10198135198135197	No Hit
CCCTTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTAGTCACAGTA	14	0.10198135198135197	No Hit



Adapter Content

